WHAT IS CLAIMED IS:

1. An isolated nucleic acid encoding a polypeptide monomer comprising an alpha subunit of a potassium channel, the polypeptide monomer:

(i) forming, with at least one additional Kir alpha subunit, a potassium channel having the characteristic of inward rectification;

(ii) having a monomer tail region that has greater than 80% amino acid sequence identity to a human Kir5.1 tail region; and

(iii) specifically binding to polyclonal antibodies generated against SEQ ID NO:1.

2. The isolated nucleic acid of claim 1, wherein the nucleic acid encodes human Kir5.1.

3. The isolated nucleic acid of claim 1, wherein the nucleic acid encodes SEQ ID NO:1.

4. The isolated nucleic acid sequence of claim 1, wherein the nucleic acid has a nucleotide sequence of SEQ ID NO:2.

5. The isolated nucleic acid of claim 1, wherein the nucleic acid is amplified by primers that selectively hybridize under stringent hybridization conditions to the same sequence as the primers selected from the group consisting of:

5' CCT AAG GGC ACA GCA AAG AAT GAG 3' (SEQ ID NO:3) and

5' GTG TGG CGA AAG TGG TGG TC 3' (SEQ ID NO:4).

6. The isolated nucleic acid of claim 1, wherein the nucleic acid encodes a polypeptide monomer having a molecular weight of about between 38 kDa to 48 kDa.

7. The isolated nucleic acid of claim 1, wherein the polypeptide monomer comprises an alpha subunit of a heteromeric inward rectifier potassium channel.

8. An isolated nucleic acid encoding a polypeptide monomer that specifically hybridizes under stringent conditions to SEQ ID NO:2.

9. The isolated nucleic acid of claim 1, wherein said nucleic acid selectively hybridizes under moderately stringent hybridization conditions to a nucleotide sequence of SEQ ID NO:2.

10. An isolated polypeptide monomer comprising an alpha subunit of a potassium channel, the polypeptide monomer:

(i) forming, with at least one additional Kir alpha subunit, a potassium channel having the characteristic of inward rectification;

(ii) having a monomer tail region that has greater than 80% amino acid sequence identity to amino acids 351-383 of a human Kir5.1 tail region; and

(iv) specifically binding to polyclonal antibodies generated against SEQ ID NO:1.

11. The isolated polypeptide monomer of claim 10, wherein the polypeptide monomer has an amino acid sequence of human Kir5.1.

12. The isolated polypeptide monomer of claim 10, wherein the polypeptide monomer has an amino acid sequence of SEQ ID NO:1.

13. The isolated polypeptide monomer of claim 10, wherein the polypeptide monomer comprises an alpha subunit of a heteromeric potassium channel.

14. An antibody that selectively binds to the polypeptide monomer of claim 10.

15. An antibody of claim 14, wherein the polypeptide monomer has an amino acid sequence of SEQ ID NO:1.

16. An expression vector comprising the nucleic acid of claim 1.

17. A host cell transfected with the vector of claim 16.

18. A method for identifying a compound that modulates ion flux through an inward rectifier potassium channel, the method comprising the steps of:

(i) contacting the compound with a eukaryotic host cell or cell membrane in which has been expressed a polypeptide monomer comprising an alpha subunit of a potassium channel, the polypeptide monomer:

(a) forming, with at least one additional Kir alpha subunit, a potassium channel having the characteristic of inward rectification;

(b) having a monomer tail region that has greater than 80% amino acid sequence identity to a human Kir5.1 tail region; and

(c) specifically binding to polyclonal antibodies generated against SEQ ID NO:1; and

(ii) determining the functional effect of the compound upon the cell or cell membrane expressing the potassium channel.

19. The method of claim 18, wherein the functional effect is determined by measuring changes in current or voltage.

20. The method of claim 18, wherein the potassium channel monomer polypeptide is recombinant.

21. The method of claim 18, wherein the potassium channel is heteromeric.

22. The method of claim 18, wherein the potassium channel monomer polypeptide is human Kir5.1.

23. The method of claim 18, wherein the potassium channel monomer polypeptide has an amino acid sequence of SEQ ID NO:1.

24. A method of detecting the presence of human Kir5.1 in mammalian tissue, the method comprising the steps of:

(i) isolating a biological sample;

(ii) contacting the biological sample with a Kir5.1-specific reagent that selectively associates with human Kir5.1; and,

(iii) detecting the level of Kir5.1-specific reagent that selectively associates with the sample.

25. The method of claim 24, wherein the Kir5.1-specific reagent is selected from the group consisting of: Kir5.1 specific antibodies, Kir5.1 specific oligonucleotide primers, and Kir5.1 nucleic acid probes.

26. The method of claim 24, wherein the sample is from a human.

27. In a computer system, a method of screening for mutations of human Kir5.1 genes, the method comprising the steps of:

(i) entering into the computer system a first nucleic acid sequence encoding an inward rectifier potassium channel polypeptide monomer having a nucleotide sequence of SEQ ID NO:2, and conservatively modified versions thereof;

(ii) comparing the first nucleic acid sequence with a second nucleic acid sequence having substantial identity to the first nucleic acid sequence; and

(iii) identifying nucleotide differences between the first and second nucleic acid sequences.

28. The method of claim 27, wherein the second nucleic acid sequence is associated with a disease state.

29. A computer readable substrate comprising the first amino acid sequence of claim 27.

30. The computer readable substrate of claim 29, further comprising the second amino acid sequence.

31. In a computer system, a method for identifying a three-dimensional structure of Kir5.1 polypeptides, the method comprising the steps of:

(i) entering into the computer system an amino acid sequence of at least 10 amino acids of a potassium channel monomer or at least 30 nucleotides of a gene encoding the polypeptide, the polypeptide having an amino acid sequence of SEQ ID NO:1, and conservatively modified versions thereof; and

(ii) generating a three-dimensional structure of the polypeptide encoded by the amino acid sequence.

32. The method of claim 31, wherein said amino acid sequence is a primary structure and wherein said generating step includes the steps of:

(i) forming a secondary structure from said primary structure using energy terms determined by the primary structure; and

(ii) forming a tertiary structure from said secondary structure using energy terms determined by said secondary structure.

33. The method of claim 31, wherein said generating step further includes the step of forming a quaternary structure from said tertiary structure using anisotrophic terms encoded by the tertiary structure.

34. The method of claim 31, further comprising the step of identifying regions of the three-dimensional structure of the protein that bind to ligands and using the regions to identify ligands that bind to the polypeptide.

35. A computer readable substrate comprising the three dimensional structure of the polypeptide of claim 31.